3. (As filed) The method according to claim 2, wherein prior to analysis, the locus at which the allele is situated is amplified.

4. (As filed) The method according to claim 3, wherein the amplification is by the PCR.

5. (As filed) The method according to any one of claims 1 to 4, wherein the locus at which the allele is situated comprises microsatellite repeats of variable lengths.

6. (As filed) The method according to claim 5, wherein amplification is performed using a pair of primers each of which hybridizes under suitably stringent conditions to a region either side of the microsatellite repeats.

A1

7. (Amended) The method according to [any one of] claim[s] 1 [to 6], wherein the allele for identification is D2S308*3.

8. (Amended) The method according to [any one of] claim[s] 3 [to 7], wherein the analysis is carried out by size separation of amplification products.

9. (As filed) The method according to claim 6, wherein the primers in the pair of primers comprise the oligonucleotide sequences identified by SEQ ID NO: 1 and SEQ ID NO: 2 or substantially similar sequences.

10. (As filed) A pair of oligonucleotide primers for amplification of an allele which is associated with asthma, which allele is situated at a locus in a region of chromosome 2 of up to 1 megabase in length, which region contains the locus D2S308.

11. (As filed) The pair of oligonucleotide primers according to claim 10, one of which is labeled with a detectable marker.

A2

12. (Amended) The pair of oligonucleotides according to claim 10 [or claim 11], capable of hybridizing under suitably stringent conditions to a region either side of a region of microsatellite repeats at D2S308.

13. (As filed) The pair of oligonucleotide primers according to claim 12, comprising the oligonucleotide sequences identified by SEQ ID NO: 1 and SEQ ID NO: 2 or substantially similar sequences.